Serial No.: 08/896,589
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In the Claims:

Please cancel claims 36 to 42, 44 to 46 and 48 to 51 without prejudice and enter the following claims 52 through 82:

52. An isolated polynucleotide comprising (a) a first polynucleotide sequence having at least 70% identity relative to a reference polynucleotide which encodes the amino acid sequence set forth in SEQ ID NO:2, or (b) the complement of the entire length of such first polynucleotide sequence, wherein having at least 70% identity means that the first polynucleotide sequence has a number, n_n, which can be zero, of altered, deleted, inserted or otherwise non-matching nucleotides when compared with the reference polynucleotide such that:

$$70\% \leq [1 - (n_n/x_n)] \times 100$$

where x_n is the total number of nucleotides in the reference sequence.

53. The isolated polynucleotide of claim 52, wherein the percent identity is calculated by an algorithm of a GCG program package.

54. The isolated polynucleotide of claim 52, wherein the percent identity is at least 95%.

55. The isolated polynucleotide of claim 54, wherein the first polynucleotide sequence encodes a Xanthine phosphoribosyl transferase polypeptide.

56. The isolated polynucleotide of claim 52, wherein the isolated polynucleotide is the complement sequence, which is the complement of the first polynucleotide sequence wherein the percent identity is at least 95%.

57. The isolated polynucleotide of claim 56, wherein the first polynucleotide sequence encodes a Xanthine phosphoribosyl transferase polypeptide.

58. The isolated polynucleotide of claim 52 comprising a polynucleotide sequence having at least a 70% identity relative to a reference polynucleotide encoding the same mature polypeptide expressed by the Xanthine phosphoribosyl transferase gene contained in *Streptococcus pneumoniae 0100993 contained in NCIMB Deposit No. 40794*.

59. A vector comprising the polynucleotide of Claim 52.

60. A host cell comprising the vector of Claim 59.

61. A process for producing a Xanthine phosphoribosyl transferase polypeptide comprising the step of culturing the host of claim 60 under conditions sufficient for the production of said polypeptide.

62. An isolated polynucleotide of claim 52, wherein the percent identity is at least 80%, or the complement of the entire length of such polynucleotide sequence.

63. An isolated polynucleotide of claim 52 wherein the percent identity is at least 90%, or the complement of the entire length of such polynucleotide sequence.

64. An isolated polynucleotide of claim 52 wherein the percent identity is at least 95%, or the complement of the entire length of such polynucleotide sequence.

65. An isolated polynucleotide comprising a first polynucleotide sequence having at least 80% identity relative to a reference polynucleotide encoding the same mature polypeptide, MPP, expressed by the Xanthine phosphoribosyl transferase gene contained in *Streptococcus pneumoniae 0100993 contained in NCIMB Deposit No. 40794*, or the complement of the entire length of such first polynucleotide sequence, wherein having at least the 80% identity means that the first polynucleotide sequence has a number, n_n, which can be zero, of altered, deleted, inserted or otherwise non-matching nucleotides when compared with the reference polynucleotide such that:

$$80\% \leq [1 - (n_n/x_n)] \times 100$$

where x_n is the total number of nucleotides in the reference sequence.

66. An isolated polynucleotide of claim 65, wherein the percent identity is at least 90%, or the complement of the entire length of such polynucleotide sequence.

67. An isolated polynucleotide of claim 65, wherein the percent identity is at least 95%, or the complement of the entire length of such polynucleotide sequence.

68. An isolated polynucleotide of claim 65 comprising a first polynucleotide sequence encoding the same mature polypeptide expressed by the Xanthine phosphoribosyl transferase gene contained in *Streptococcus pneumoniae 0100993 contained in NCIMB Deposit No. 40794*, or the complement of the entire length of such first polynucleotide sequence.

69. A recombinant polynucleotide comprising the nucleotide sequence from position 1 to 579 inclusive of the polynucleotide sequence set forth in SEQ ID NO:1, or the complement of the entire length of such position 1 to 579 polynucleotide sequence.

70. A recombinant polynucleotide which encodes a polypeptide comprising a region having the amino acid sequence of SEQ ID NO:2, or the complement of the entire length of the encoding polynucleotide sequence.

71. A vector comprising the polynucleotide of Claim 70.

72. A host cell comprising the vector of Claim 71.

73. A process for producing a Xanthine phosphoribosyl transferase polypeptide comprising the step of culturing a host of claim 72 under conditions sufficient for the production of said polypeptide.

74. An isolated polynucleotide comprising a first polynucleotide sequence having at least 70% identity relative to a reference polynucleotide having the sequence of SEQ ID NO: 1, and which hybridizes under stringent conditions to said reference polynucleotide, or the complement of the entire length of such polynucleotide sequence, wherein having at least 70% identity means that the first polynucleotide sequence has a number, n_n, which can be zero, of altered, deleted, inserted or otherwise non-matching nucleotides when compared with the reference polynucleotide such that:

$$70\% \leq [1 - (n_n/x_n)] \times 100$$

where x_n is the total number of nucleotides in the reference sequence.

75. An isolated polynucleotide of claim 74, wherein the percent identity is at least 80%, or the complement of the entire length of such polynucleotide sequence.

76. An isolated polynucleotide of claim 74, wherein the percent identity is at least 90%, or the complement of the entire length of such polynucleotide sequence.

77. An isolated polynucleotide of claim 74, wherein the percent identity is at least 95%, or the complement of the entire length of such polynucleotide sequence.

78. An isolated polynucleotide comprising a first polynucleotide sequence having at least 70% identity relative to a first reference polynucleotide that encodes the polypeptide sequence of SEQ ID NO:2, and which hybridizes under stringent conditions to a second reference polynucleotide having the sequence of SEQ ID NO:1, or the complement of the entire length of given such polynucleotide sequence, having at least 70% identity means that the first polynucleotide sequence has a number, n_n, which can be zero, of altered, deleted, inserted or otherwise non-matching nucleotides when compared with the reference polynucleotide such that:

$$70\% \leq [1 - (n_n/x_n)] \times 100$$

where x_n is the total number of nucleotides in the reference sequence.